Claims

1. An oligonucleotide as alpha-arteether resistance domain (ADR) of SEQ ID No. 1.

2. An oligonucleotide as alpha-arteether resistance domain (ADR) as claimed in claim 1, wherein the domain is from 241 to 261 nucleotide position of *gyr* A gene from translation start site of *E. Coli.*

3. An oligopeptide of SEQ ID No. 2, corresponding to an oligonucleotide as alpha-arteether resistance domain (ADR) of SEQ ID No. 1.

4. An oligopeptide as claimed in claim 3, wherein the oligopeptide is from amino acid position 81 to 87 in *gyrase* A peptide of the enzyme.

5. A method of identifying alpha-arteether resistance domain (ADR) in a alpha-arteether resistant pathogens, to help develop drugs against the pathogen, said method comprising steps of:

    a. developing alpha-arteether resistant mutant from arteether sensitive strain,

    b. identifying both phenotypic and genotypic characteristics of the developed alpha-arteether resistant mutant, and

    c. identifying alpha-arteether resistance domain (ADR) in an alpha-arteether resistant pathogens.

6. A method as claimed in claim 5, wherein an alpha-arteether resistance domain (ADR) is an oligonucleotide of SEQ ID No. 1

7. A method as claimed in claim 5, wherein the ADR is from 241 to 261 nucleotide position of *gyr* A gene from translation start site of *E. Coli.*

8. A method as claimed in claim 5, wherein the ADR has corresponding an oligopeptide of SEQ ID No. 2.

9. A method as claimed in claim 8, wherein the oligopeptide is from amino acid position 81 to 87 in *gyrase* A peptide of the enzyme.

10. A set of three pairs of primers of SEQ ID Nos. 3, 4; 5, 6; and 7, 8.

11. A set of primers as claimed in claim 10, wherein the primers of SEQ ID Nos 3, 5, and 7 are forward primers.

12. A set of primers as claimed in claim 10, wherein the primers of SEQ ID Nos 4, 6, and 8 are reverse primers.